Claims:

1. A method of isolating a cytoplasmic fraction from an oocyte which does not impair the capacity of the oocyte to be fertilized, the method including the step of releasing a cytoplasmic fraction from the oocyte which is about 5% of the volume of the oocyte.

2. A method according to claim 2, wherein the fraction is about 2% of the volume of the oocyte.

3. A method according to claim 1 including the following steps:

(a) inserting releasing means into the oocyte;

(b) drawing a cytoplasmic fraction which is about 5% of the volume of the oocyte into the releasing means; and

(c) withdrawing the releasing means from the oocyte so that the fraction is isolated in the releasing means.

4. A method according to claim 3 wherein the volume of the fraction is less than 10pL.

5. A method according to claim 4 wherein the volume of the fraction is equal to the volume of oocyte cytoplasm which can be drawn about 100μm into an intra cytoplasmic sperm injection (ICSI) pipette.

6. A method according to claim 1 wherein the cytoplasmic fraction includes mitochondria.

7. A method according to claim 3 wherein the releasing means includes an injection pipette.

8. A method according to claim 7 wherein the injection pipette is an ICSI pipette.

9. A method of detecting a nucleotide sequence, polymorphism or mutation in the mitochondrial genome of mitochondria located in an oocyte which does not impair the capacity of the oocyte to be fertilized, the method including the following steps:

(a) isolating a cytoplasmic fraction which includes mitochondria from the oocyte according to the method of claim 1; and

(b) analysing the nucleotide sequence of the mitochondrial genome of the mitochondria in the cytoplasmic fraction for the presence of a nucleotide sequence, polymorphism or mutation in the mitochondrial genome.

10. A method according to claim 9 wherein the nucleotide sequence, polymorphism or mutation is one which causes, or is suspected of causing, or is associated with, a disease or dysfunction in the oocyte, or in the progeny descended from the fertilized oocyte.

11. A method according to claim 10 wherein the nucleotide sequence, polymorphism or mutation is shown in Table 1.

12. A method of determining the level of heteroplasmy of mitochondrial genomes in an oocyte which does not impair the capacity of the oocyte to be fertilized, the method including the following steps:

(a) isolating a cytoplasmic fraction which includes mitochondria from the oocyte according to the method of claim 1; and

(b) comparing the number of mitochondrial genomes in the fraction with a nucleotide sequence, polymorphism or mutation, with the number of genomes without the nucleotide sequence, polymorphism or mutation in the fraction.

13. A method according to claim 12 wherein the oocyte from which the cytoplasmic fraction is isolated is a primary oocyte at the germinal vesicle stage of oocyte development, or a secondary oocyte at a stage of oocyte

development from the metaphase II stage of meiosis to prior to syngamy.

14. A method according to claim 13 wherein the nucleotide sequence, polymorphism or mutation of the mitochondrial genome is one which causes, or is suspected of causing, or is associated with, a disease or dysfunction in the oocyte or in progeny descended from the fertilized oocyte.

15. A method according to claim 14 wherein the nucleotide sequence, polymorphism or mutation is shown in Table 1.

16. A method of isolating a cytoplasmic fraction from an embryonic cell which does not impair the developmental potential of the cell, the method including the step of releasing a cytoplasmic fraction from the cell which is about 5% of the volume of the cell.

17. A method according to claim 16 wherein the fraction is about 2% of the volume of the cell.

18. A method according to claim 16 including the following steps:

(a) inserting releasing means into the embryonic cell;

(b) drawing a cytoplasmic fraction which is about 5% of the volume of the cell into the releasing means; and

(c) withdrawing the releasing means from the cell so that the fraction is isolated in the releasing means.

19. A method according to claim 18 wherein the volume of the fraction is less than 10pL.

20. A method according to claim 19 wherein the volume of the fraction is equal to the volume of embryonic cell cytoplasm which can be drawn about 100μm into an ICSI pipette.

21. A method according to claim 16 wherein the cytoplasmic fraction includes mitochondria.

22. A method according to claim 18 wherein the releasing means includes an injection pipette.

23. A method according to claim 22 wherein the injection pipette is an ICSI pipette.

24. A method of detecting a nucleotide sequence, polymorphism or mutation in the mitochondrial genome of mitochondria located in an embryonic cell which does not impair the developmental potential of the cell, the method including the following steps:

(a) isolating a cytoplasmic fraction which includes mitochondria from the embryonic cell according to the method of claim 16; and

(b) analysing the nucleotide sequence of the mitochondrial genome of the mitochondria in the cytoplasmic fraction for the presence of a nucleotide sequence, polymorphism or mutation in the mitochondrial genome.

25. A method according to claim 24 wherein the nucleotide sequence, polymorphism or mutation is one which causes, or is suspected of causing, or is associated with, a disease or dysfunction in the embryonic cell, or in the progeny descended from the embryonic cell.

26. A method according to claim 25 wherein the nucleotide sequence, polymorphism or mutation is shown in Table 1.

27. A method of determining the level of heteroplasmy of mitochondrial genomes in an embryonic cell which does not impair the developmental potential of the cell, the method including the following steps:

(a) isolating a cytoplasmic fraction which includes mitochondria from the embryonic cell according to the method of claim 16; and

(b) comparing the number of mitochondrial genomes in the fraction with a nucleotide sequence, polymorphism or mutation, with the number of genomes without the nucleotide sequence, polymorphism or mutation in the fraction.

28. A method according to claim 27 wherein the nucleotide sequence, polymorphism or mutation of the mitochondrial genome is one which causes, or is suspected of causing, or is associated with, a disease or dysfunction in the embryonic cell, or in progeny descended from the cell.

29. A method according to claim 28 wherein the nucleotide sequence, polymorphism or mutation is shown in Table 1.